AMENDMENTS TO THE SPECIFICATION

Please replace the sequence alignment table beginning on page 16, line 13, and bridging to page 18, line 34, with the following amended sequence alignment table:

Nucleic acid alignment for SEQ ID NOS. 1, 3, 5, 7, and 9:

```
1                                                         50
        CanA    (1)  GTGAAGTACACAACCCTAGCTATAGCGGGTATTATTGCCTCGGCTGCCGC
        CanB    (1)  GTGAAGCCTACGGCTCTAGCCCTGGCTGGTATCATTGCCTCGGCTGCCGA
        CanC    (1)  ATGAGGTACACGACCCTAGCTCTGGCCGGCATAGTGGCCTCGGCTGCCGC
CanD_partial    (1)  -------------------------------------------------
CanE_partial    (1)  -------------------------------------------------
   Consensus    (1)   TGA G   AC  C CTAGC  T GC GG AT  T GCCTCGGCTGCCG
                                                          51                                                       100
        CanA   (51)  CCTCGCCCTCCTAGCAGGCTTCGCCACCACCCAGAGCCCCCTCAACAGCT
        CanB   (51)  CCTCGCCCTGCTAGCAGGCTTCGCCACCACCCAGAGCCCGCTCAACAGCT
        CanC   (51)  CCTCGCCCTGCTAGCAGGCTTCGCCACGACCCAGAGCCCGCTAAGCAGCT
CanD_partial    (1)  ---------------------------------------------AGCT
CanE_partial    (1)  ---------------------------------------------AGCT
   Consensus   (51)  CCTCGCCCT CTAGCAGGCTTCGCCAC ACCCAGAGCCC CT A CAGCT
                                                          101                                                      150
        CanA  (101)  TCTACGCCACCGGTACAGCACAGGCAGTAAGCGAGCCAATAGACGTAGAA
        CanB  (101)  TCTACGCCACCGGCACAGCAGCCGCAACAAGCGAGCCAATAGACGTAGAG
        CanC  (101)  TCTACGCCACCGGCACAGCACAAGCAGTAAGCGAGCCAATAGACGTAGAG
CanD_partial    (5)  TCTACGCCACCGGCACAGCACAGGCAGTAAGCGAGCCAATAGACGTGGTA
CanE_partial    (5)  TCTACGCCACCGGCACAGCAGAGGCAACAAGCGAGCCAATAGACGTTGTA
   Consensus  (101)  TCTACGCCACCGGCACAGCACAGGCAGTAAGCGAGCCAATAGACGTAGAA
                                                          151                                                      200
        CanA  (151)  AGCCACCT---CGGCAGCATAACCCCCGCAGCCGGCGCACAGGGCAGTGA
        CanB  (151)  AGCCACCT---CAGCAGCATAGCCCCTGCTGCTGGCGCACAGGGCAGCCA
        CanC  (151)  AGCCACCTAGACAACACCATAGCCCCTGCTGCCGGTGCACAGGGCTACAA
CanD_partial   (55)  AGCAGCCTCGGTACG---CTAAATACTGCCGCTGGTGCACAGGGTAAGCA
CanE_partial   (55)  AGCAACCTTAACACGGCCATAGCCCCTGCTGCCGGCGCCCAGGGCAGCGT
   Consensus  (151)  AGCCACCT  CA CA CATAGCCCCTGCTGCCGGCGCACAGGGCAGC A
                                                          201                                                      250
        CanA  (198)  CGACATAGGTTACGCAATAGTGTGGATAAAGGACCAGGTCAATGATGTAA
        CanB  (198)  GGACATAGGCTACTTCAACGTGACCGCCAAGGATCAAGTGAACGTGACAA
        CanC  (201)  GGACATGGGCTACATTAAGATAACTAACCAGTCAAAAGTTAATGTAATAA
CanD_partial  (102)  GACGCTAGGAGACATAACAATATATGCGCACAATGACGTGAACATAACAA
CanE_partial  (105)  GGGCATAGGCAGCATAACAATAGAGAACAAGACTGACGTGAACGTTGTGA
   Consensus  (201)  GGACATAGGCTACATAA AATA  A CAAG AT A GTGAACGT ATAA
                                                          251                                                      300
        CanA  (248)  AGCTGAAGGTGACCCTGCGTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
        CanB  (248)  AGATAAAGGTGACCCTGGCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
        CanC  (251)  AGCTGAAGGTGACTCTCGCTAACGCCGAGCAGCTAAAGCCCTACTTCGAC
CanD_partial  (152)  AGCTAAAGGTCACGCTTGCTAACGCTGCACAGCTAAGACCATACTTCAAG
CanE_partial  (155)  AGCTGAAGATAACCCTCGCCAACGCTGAGCAGCTAAAGCCCTACTTCGAC
   Consensus  (251)  AGCTGAAGGTGACCCT GCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
                                                          301                                                      350
        CanA  (298)  TACCTACAGATACAGATAACAAGCGGCTATGAGACGAACAGCACAGCTCT
        CanB  (298)  TACCTACAGATAGTGCTAAAGAGCG-------------------------
        CanC  (301)  TACCTACAGCTAGTACTCACAAGCAAC-----------------GCCAC
CanD_partial  (202)  TACCTGATAATAAAGCTAGTAAGCCT-------------GGACAGC-AA
CanE_partial  (205)  TACCTACAGATAGTGCTAAAGAGCGT-------------TGACAGC-AA
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```
Consensus   (301) TACCTACAGATAGTGCTAA AAGCG                    ACAGC A
                  351                                                 400
       CanA  (348) AGGCAACTTCAGCGAGACCAAGGCTGTGATAAGCCTCGACAACCCCAGCG
       CanB  (323) AGGTAGCTGA--CGAGATCAAGGCCGTAATAAGCATAGACAAGCCTAGCG
       CanC  (333) TGGCACCGACA---TGGTTAAGGCTGTGCTAAGCCTCGAGAAGCCTAGCG
CanD_partial  (237) CGGCAACGAGTCCGAGGAAAAGGGCATGATAACTCTATGGAAGCCTTACG
CanE_partial  (240) CGAGATCAAGGCTG------------TGCTAAGCCTCGAGAAGCCCAGCG
   Consensus  (351)  GGCA C A   CGAG   AAGGC GTGATAAGCCTCGAGAAGCCTAGCG
                  401                                                 450
       CanA  (398) CCGTGATAGTACTAGACAAGGAGGATATAGCAGTGCTCTATCCGGACAAG
       CanB  (371) CCGTCATAATACTAGACAGCCAGGA-------------------------
       CanC  (380) CAGTCATAATACTAGACAACGATGA-------------------------
CanD_partial  (287) CCGTGATAATACTAGACCATGAAGA-------------------------
CanE_partial  (278) CAGTCATAATACTGGACAACGAGGA-------------------------
   Consensus  (401) CCGTCATAATACTAGACAACGAGGA
                  451                                                 500
       CanA  (448) ACCGGTTACACAAACACTTCGATATGGGTACCCGGTGAACCTGACAAGAT
       canB  (396) ----------------CTTCGACA-------------G-----------
       CanC  (405) ----------------CTACGATA-------------G-----------
canD_partial  (312) ----------------TTTCAACAACGACA-------------------
canE_partial  (303) ----------------CTTCCAGGGCGGC-------------------
   Consensus  (451)                CTTCGA A   G
                  501                                                 550
       CanA  (498) AATTGTCTACAACGAGACAAAGCCAGTAGCTATACTGAACTTCAAGGCCT
       canB  (405) ------CAACAACAGAGCAAAG--ATAAGCGCCACTG---------CCT
       CanC  (414) ------CACTAACAAGATACAGCTA-AAGGTAGA---A--------G-CCT
canD_partial  (326) -----TCGACAATGACGGCAACAATGACGCCAAGATAAGGGTTGTAGCCT
canE_partial  (316) -------GACAACCAGTGCCAGATAGACGCCACC-----------GCCT
   Consensus  (501)     C ACAAC AG  AAAG  AGAAGC A A T A       GCCT
                  551                                                 600
       CanA  (548) TCTACGAGGCTAAGGAGGGTATGCTATTCGACAGCCTGCCAGTGATATTC
       canB  (437) ACTACGAGGCTAAGGAGGGCATGCTATTCGACAGCCTACCGCTAATATTC
       CanC  (446) ACTATGAGGCTAAGGAGGGCATGCTATTCGACAGCCTACCAGTAATACTG
canD_partial  (371) ACTATGAGGCTAAGGAGGGTATGCT-------------------------
canE_partial  (347) ACTACGAGGCTAAGGAGGGTATGCTA------------------------
   Consensus  (551) ACTACGAGGCTAAGGAGGGTATGCTATTCGACAGCCT CC  T ATA T
                  601                                  642
       CanA  (598) AACTTCCAGGTGCTACAAGTAGGCTAA---------------
       canB  (487) AACATACAGGTGCTAAGCGTCAGCTAA---------------
       CanC  (496) AACTTCCAGGTACTGAGCGCCGCTTGCAGTCCCTTGTGGTGA
canD_partial  (396) ------------------------------------------
canE_partial  (373) ------------------------------------------
   Consensus  (601) AAC T CAGGT CT   G     T
```

Amino Acid Alignment for SEQ ID NOS. 2, 4, 6, 8, and 10:

```
1                                           50
   CanA_pep   (1) VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVE
   CanB_pep   (1) VKPTALALAGIIASAADLALLAGFATTQSPLNSFYATGTAAATSEPIDVE
   CanC_pep   (1) MRYTTLALAGIVASAAALALLAGFATTQSPLSSFYATGTAQAVSEPIDVE
CanD_partial  (1) ------------------------------SFYATGTAQAVSEPIDVV
CanE_partial  (1) ------------------------------SFYATGTAEATSEPIDVV
   Consensus  (1) VK T LALAGIIASAA LALLAGFATTQSPL SFYATGTAQAVSEPIDVE
                  51                                          100
   CanA_pep  (51) SHLG-SITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFK
   CanB_pep  (51) SHLS-SIAPAAGAQGSQDIGYFNVTAKDQVNVTKIKVTLANAEQLKPYFK
   CanC_pep  (51) SHLDNTIAPAAGAQGYKDMGYIKITNQSKVNVIKLKVTLANAEQLKPYFD
CanD_partial  (19) SSLGTLNT-AAGAQGKQTLGDITIYAHNDVNITKLKVTLANAAQLRPYFK
```

```
CanE_partial    (19)  SNLNTAIAPAAGAQGSVGIGSITIENKTDVNVVKLKITLANAEQLKPYFD
   Consensus    (51)  SHL  SIAPAAGAQGS DIGYI I  K  VNVVKLKVTLANAEQLKPYFK
                      101                                              150
      CanA_pep   (100) YLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDK
      CanB_pep   (100) YLQIVLKSEVAD---------EIKAVISIDKPSAVIILDSQDFDSNNR--
      CanC_pep   (101) YLQLVLTSNATG-------TDMVKAVLSLEKPSAVIILDNDDYDSTN---
CanD_partial    (68)  YLIIKLVSLDSNG-----NESEEKGMITLWKPYAVIILDHEDFNNDID--
CanE_partial    (69)  YLQIVLKSVDSN---------EIKAVLSLEKPSAVIILDNEDFQG-----
   Consensus    (101) YLQIVL S  S         EIKAVISLDKPSAVIILD EDF
                      151                                              200
      CanA_pep   (150) TGYTNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGMLFDSLPVIF
      CanB_pep   (139) -----------------------AKISATAYYEAKEGMLFDSLPLIF
      CanC_pep   (141) ---------------KIQ---------LKVEAYYEAKEGMLFDSLPVIL
CanD_partial    (111) ------------------N--DGNNDAKIRVVAYYEAKEGM---------
CanE_partial    (105) --------------------GDNQCQIDATAYYEAKEGML--------
   Consensus    (151)                         A I   AYYEAKEGMLFDSLPVI
                      201         214
      CanA_pep   (200) NFQVLQVG------
      CanB_pep   (163) NIQVLSVS------
      CanC_pep   (166) NFQVLSAACSPLW-
CanD_partial    (132) --------------
CanE_partial    (125) --------------
   Consensus    (201) N QVL
```